

OM of: US-08-711-417c-165 to: Issued_Patents_AA.* out_format : pfs

Date: Aug 28, 2002 10:02 AM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

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Search information block:

Query: US-08-711-417c-165

Query length: 1551

Database: Issued_Patents_AA

Database sequences: 231628

Search time (sec): 24425594

Search time (sec): 34.160000

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seq_documentation_block:

: Sequence 202, Application US/08711417C

: Patent No. 6228611

: GENERAL INFORMATION:

: APPLICANT: Georgopoulos, Katia A.

: TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE

: NUMBER OF SEQUENCES: 202

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Fish & Richardson P.C.

: STREET: 225 Franklin Street

: CITY: Boston

: STATE: MA

: COUNTRY: USA

: ZIP: 02110-2804

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Diskette

: COMPUTER: IBM Compatible

: OPERATING SYSTEM: Windows 95

: SOFTWARE: FastSeq for Windows Version 2.0b

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/08/711,417C

: FILING DATE: 05-Sep-1996

: PRIORITY INFORMATION:

: APPLICATION NUMBER: 08/238,212

: FILING DATE: 02-MAY-1994

: APPLICATION NUMBER: 08/121,438

: FILING DATE: 14-SEP-1993

: APPLICATION NUMBER: 07/946,233

: FILING DATE: 14-SEP-1992

: ATTORNEY/AGENT INFORMATION:

: NAME: Myers, Louis P.

: REGISTRATION NUMBER: 35,965

: REFERENCE/DOCKET NUMBER: 10287/007001

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: 617/542-5070

: TELEFAX: 617/542-8906

: TELEX: 200154

: INFORMATION FOR SEQ ID NO: 202:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 516 amino acids

: TYPE: amino acid

: TOPOLOGY: linear

: MOLECULE TYPE: protein

: FRAGMENT TYPE: internal

: SEQUENCE DESCRIPTION: SEQ ID NO: 202:

US-08-711-417C-202

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Ratio: 5.329 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

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us-08-711-417c-165.ra1

Wed Aug 28 10:05:45 2002

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seq_documentation_block:
; Sequence 196, Application US/08711417C
; Patent No. 6228611
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 202
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/711.417C
; FILING DATE: 05-Sep-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/238,212
; FILING DATE: 02-MAY-1994
; APPLICATION NUMBER: 08/121,438
; FILING DATE: 14-SEP-1993
;
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; APPLICATION NUMBER: 07/946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis P.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10287/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 196:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 461 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 196:
US-08-711-417c-196
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; Sequence 198, Application US/08711417C
; Patent No. 6228611
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 202
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/711,417C
; FILING DATE: 05-Sep-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/238,212
; FILING DATE: 02-MAY-1994
; APPLICATION NUMBER: 08/121,438
; FILING DATE: 14-SEP-1993
; APPLICATION NUMBER: 07/946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis P.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10287/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 198:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 518 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 198:
US-08-711-417C-198

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  Percent Similarity: 95.202  Percent Identity: 89.635

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17 rProProValSerAspThrProAspGluGlyAspGluProMetProValP 34
101 CCAGGACCTCTCCACCCTCGGGAGGACAGCAAGCTCCAGAGTGAC 150
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151 AGAGTCGTGGCCAGTAATGTTAAAGTAGAGACATCAGAGTCATGAAGAGAA 200
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51 ArgGlyMetAlaSerAsnValLysValGluThrGlnSerAspGluLys 67

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117 uLysCysAspIleCysGlyIleValCysIleGlyProAsnValLeuMetV 134
401 TTCACAAAAGAACCCACACTGGAGAACGGCCCTTCCAGTGCATCAGTGC 450
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
134 aHisLysArgSerHisThrGlyGluArgProPheGlnCysAsnGlnSer 150
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451 GGGCGCTCATTCACCCAGAGGCAACCTGCTCCGGCACATCAAGCTGCA 500
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151 GlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuH 167
501 TTCGGGGAGAACCCCTTCAATGCCACCTCTGCAACTAGCCCTGCGGCC 550
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167 sSerGlyGluLysProPheLysCysHisLeuCysAsnTyrAlaCysArg 184
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651 GGAACATAAGACGCGCTGCCAACACTACTTTGGAAAGCATGGGCTTCCGG 700
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234 ly...ValCysProValIleLysGluGluThrAsnHisAsnGluMetAla 249
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751 GAAGACCTGTGCAAGATAGATCAGAGAGATCTCTCGTGTGACAGACT 800
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801 AGCAAGTAATGTGCCAAACGTAAAGACTCTATGCTCAGAAATTTCTTG 850
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266 uAlaSerAsnValAlaLysArgLysSerSerMetProGlnLysPheLeu 283
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851 GGGCAAGGGCTGTCCGACACGCCCTACACAGCTGCCAGTACGAGAAG 900
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
283 lyAspLysCysLeuSerAspMetProTyrAspSerAlaAsnTyrGluLys 299
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901 GAGAACGAAATGATGAAGTCCACGCTGATGGACCAAGCCCATCAACACG 950
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300 Glu...AspMetMetThrSerHisValMetAspGlnAlaIleAsnAl 315
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951 CATCAACTACCTGGGGCGGAGTCCCTGCGCCCGCTGGTGCACAGCCGCC 1000
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315 aIleAsnTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThrProp 332
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1001 CGGGCGGTTCCGAGGTGGTCCCGGTTCATACAGCCCGATGTACCAAGCTGCAC 1050
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332 roGlySerSerGluValValProValIleSerSerMetTyrGlnLeuHis 348
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701 GCACACTGACCCAGTCATTAAGAAGAACTAAGCAGAGTGAATGGCA 750
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284 ly...MetTyrProValIleLysGluThrAsnHisAsnGluMetAla 299
751 GAAGACCTGTGCAAGATAGATCAGAGAGATCTCGTCTGGACAGACT 800
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300 GluAspLeuCysLysIleGlyAlaGluArgSerLeuValLeuAspArgLe 316
801 AGCAAGTAATGTGCCAAACGTAAGAGCTCTATGCTTCAGAAATTTCTG 850
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851 GGCACAGGGCTGTCGACAGCCCTCAGCAGTGCACAGTCCACGAGAG 900
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1098 CGCGGTGAGTACTCTCTCTCTCTCAGGCGCAAGTTGGTCCCTCGG 1147
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415 .AlaValAspAsnLeuLeuLeuSerLysAlaLysSerValSerSerg 431
1148 AGCGCGAGGCGTCCCGAGCAACAGCTGCCAAGCTCCACGCGACCCGAG 1197
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431 luArgGluAlaSerProSerAsnSerCysGlnAspSerThrAspThrGlu 447
1198 AGCAACAACGAGGAGGAGCGCGCTCTTACTACCTGACCAACACAT 1247
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464 eAsnProHisAlaArgAsnGlyLeuAlaLeuLysGluGluGlnArgAla 481
1295 AGGACCTGCTGCGCGCGCTCGAGAACTCGCAGGACGCGCTCGCGCTG 1344
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481 yGluValLeuArgAlaAlaSerGluAsnSerGlnAspAlaPheArgVal 497
1345 GTCAGCACCGCGGGAGGAGATGAAGGTGTACAAGTGCAGAACTGCCG 1394
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498 ValSerThrSergGlyGluGlnLeuLysValTyrLysCysGluHisCys 514
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564 gTyrHisLeuSer 568
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seq_documentation_block:
; Sequence 153, Application US/08465590
; Patent No. 5824770
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 164
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,590
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/238,212
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,438
; FILING DATE: 14-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,695
; REFERENCE/DOCKET NUMBER: MPG-006C2DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 153:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 470 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: C-terminal
; US-08-465-590-153

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Ratio: 5.098 Gaps: 3
Percent Similarity: 92.521 Percent Identity: 90.385

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210 CTGTGAATGAATGGGAAGAATGTGCGGAGGATTTACGAATGCTTGATG 259
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19 acysGluMetAsnGlyGluGluCysAlaGluAspLeuArgMetLeuAsp 36
260 CCTCGGAGAGAAAATGAATGGCTCCCAAGGACCAAGGACGCTCGCT 309
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36 laSerGlyGluLysMetAsnGlySerHisArgAspGlnGlySerSerAla 52
310 TTGTCGGAGATTGAGGCAATTCAGCTTCTTAAAGGAAATCAAGTGTGA 359
53 LeuSerGlyValGlyGlyLeuArgLeuProAsnGlyLysLeuLysCysAs 69
360 TATCTGTGGGATCATTTGCAATCGGGCCCAATGTGCTCATGTTCAAAA 409
69 pIleCysGlyIle***CysIleGlyProAsnValLeuMetValHisLysA 86
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610 GGATATTGCGCGGAGAGCTATAACAGCAACGCTCTTTAGAGGAACATA 659
153 GlyTyrCysGlyArgSerTyrLysGlnArg***SerLeuGluGluHis 169
660 AGAGCGCTGCCACAACTACTTGAAGAGCATGGCCCTCCGGCCACACTGT 709
169 sGluArgCysHisAsnTyrLeuGluSerMetGlyLeuProGly***** 186
710 ACCAGCTATTAAAGAAGAACTAAGCAGAGTGAATGCGAAGACCTG 759
186 **ProValIleLysGluGluThr***His***GluMetAlaGluAspLeu 202
760 TGAAGATAGGATCAGAGATCTCTGCTGCTGGGACAGACTAGCAAGTAA 809
203 CysLysIleGly**GluArgSerLeuValLeuAspArgLeuAlaSerAs 219
810 TGTCCGCAACCTAAGAGCTCTATCTCTCAGAAATTTCTGGGACAAAG 859
219 nValAlaLysArgLysSerSerMetProGlnLysPheLeuGlyAspLys* 236
860 GCTGTCCGACAGCCCTACGACAGTGCACGTGCGAAGAGGAGAACAA 909
236 **LeuSerAsp***ProTyrAspSerAla***TyrGluLysGlu***** 252
910 ATGATGAAGTCCCGCTGATGGACCAAGCCATCAACAGCCATCAACTA 959
253 MetMet***SerHisValMetAsp***AlaIleAsnAsnAlaIleAsn 269
960 CTGCGGGCGGAGTCCCTGCGCGCGCTGGTGCAGACGCCCGCGCGGTT 1009
269 rLeuGlyAlaGluSerLeuArgProLeuValGlnThrProProGly***S 286
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286 rGluValValProValIleSerProMetTyrGlnLeuHis***** 302
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303 Ser***Gly***ProArgSerAsnHisSerAlaGlnAsp***AlaVal** 319
1107 GTACCTGCTGCTCTCCAGGCGCAAGTGTGGTCCCTCGAGCGCGAGG 1156
319 ***LeuLeuLeuLeuSerLysAlaLys***Val***SerGluArgGluA 336
1157 GGTCCCGGAGCAACAGCTGCGCAACACTCCAGGACACCGAGCAACAC 1206
336 laSerProSerAsnSerCysGlnAspSerThrAspThrGluSerAsn** 352
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333 GluGluGlnArgSerGlyLeuIleTyrIleThrAsnHisIle***** 369
1257 CGCG...CAACGCGGTGCTGCTCAAGGAGGAGCAGCGCTTACGACCTGC 1303
369 *Ala*****LeuLysGluGlu***ArgAlaTyr*****L 386
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419 eLeuAspHisValMetTyrThrIleHisMet*****GlyCysHisG 436
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seq_documentation_block:
; Sequence 13, Application US/08283300A
; Patent No. 6172278
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS TRANSGENIC CELLS AND ANIMALS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Ascii (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/283,300A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/238,212
; FILING DATE: 02-MAY-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,438
; FILING DATE: 14-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,695
; REFERENCE/DOCKET NUMBER: MGP-027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
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; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 470 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: C-terminal
; US-08-283-300A-13

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  Quality: 2207.50      Length: 468
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410 GAAGCCACACTGGAGAACGGCCCTTCAGTGCAATCAGTCGGGGGCTCA 459
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103 PheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHisSerGlyGI 119
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119 uLysProPheLysCysHisLeuCysAsnTyrAlaCysArgArgAspA 136
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; Sequence 13, Application PC/TUS9509345
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```
; GENERAL INFORMATION:
```

```
; APPLICANT: Georgopoulos, Katia A.
```

```
; TITLE OF INVENTION: IKAROS TRANSGENIC CELLS AND ANIMALS
```

```
; NUMBER OF SEQUENCES: 26
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```
; CORRESPONDENCE ADDRESS:
```



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1304 TGCAGCGCGCTCCGAGAACTCCAGAGCGCGCTCGCGTGGTGCACACC 1353
      |||||||
386 euArgAlaAaSerGluAsnSerGlnAspAla**ArgValValSerThr 402
      |||||||
1354 AGCGGGGAGCAGATGAAGGTGTACAGTGGACACTGCGGGTGCTCTT 1403
      |||||||
403 SerGlyGluGln**LysValTyrLysCysGluHisCysArgValLeuPh 419
      |||||||
1404 CCTGGATCAGTCATGTACACCATCCACATG.....GGCTGCCAGC 1444
      |||||||
419 eLeuAspHisValMetTyrThrIleHisMet*****GlyCysHisG 436
      |||||||
1445 GCTTCGCTGATCCTTTTGTAGTCAACATGTGGGCTACACAGCCAGGAC 1494
      |||||||
436 LyPheArgAspProPheGluCysAsnMetCysGlyTyrHisSerGlnAsp 452
      |||||||
1495 CGGTACAGTTCCTCGTCGCACATAACGCGAGGGGAGCAGCGTCCACAT 1544
      |||||||
453 ArgTyrGluPheSerSerHisIleThrArgGlyGluHisArg***His 469
      |||
1545 GAGC 1548
      |||
469 *Ser 470

seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pap:US-08-711-417C-153

seq documentation_block:
; Sequence 153, Application US/08711417C
; Patent No. 6228611
;
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 202
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/711,417C
; FILING DATE: 05-Sep-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/238,212
; FILING DATE: 02-MAY-1994
; APPLICATION NUMBER: 08/121,438
; FILING DATE: 14-SEP-1993
; APPLICATION NUMBER: 07/946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis P.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10287/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 153
; SEQUENCE CHARACTERISTICS:
; LENGTH: 470 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: C-terminal
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1...470

OTHER INFORMATION: Xaa = any amino acid
; SEQUENCE DESCRIPTION: SEQ ID NO: 153:
US-08-711-417C-153

alignment_scores:
Quality: 2202.50 Length: 468
Ratio: 5.087 Gaps: 3
Percent Similarity: 92.521 Percent Identity: 90.171

alignment_block:
US-08-711-417C-165 x US-08-711-417C-153 ..
Align seg 1/1 to: US-08-711-417C-153 from: 1 to: 470

160 GCCAGTAATGTTAAAGTAGAGACTCAGAGTGCATGAAGAGAATGGCGTGC 209
      |||||||
3 AlaSerAsnValLysValIleThrGlnSerAspGluGluAspGlyArgAl 19
      |||||||
210 CTGTCAAAATGAATGGGGAAGAATGTGCGGAGGATTTAGCAATGCTTGATG 259
      |||||||
19 acysGluMetAsnGlyGluGluCysAlaGluAspLeuArgMetLeuAsp 36
      |||||||
260 COTCGGAGAGAAAATGAATGGCTCCACAGGACCAAGGACGCTCGGCT 309
      |||||||
36 laSerGlyGluLysMetAsnGlySerHisArgAspGlnGlySerSerAla 52
      |||||||
310 TTGTCGGGAGTTGGAGCATTCGACTTCCTTAACGGAATAAAGTGTGA 359
      |||||||
53 LeuSerGlyValGlyIleArgLeuProAsnGlyLysLeuLysCysAs 69
      |||||||
360 TATCTGTGGGATCATTTGCATCGGGCCCAATGTCTCATGTGTACAAAA 409
      |||||||
69 pileCysGlyIle***CysIleGlyProAsnValLeuMetValHisLys 86
      |||||||
410 GAAGCCACACTGGAGAACGGCCCTTCCAGTGCATCAATCAGTGGGCGCTCA 459
      |||||||
86 rgSerHisThrGlyGluArgProPheGlnCysAsnGlnCysGlyAlaSer 102
      |||||||
460 TTCACCCAGAGGGCAACCTGCTCCGGCAGCATCAAGCTGCATTCGGGGA 509
      |||||||
103 PheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHisSerGly 119
      |||||||
510 GAAGCCCTTCAATGCCACTCTGCACTACGCCCTGCGCGCGGAGGACG 559
      |||||||
119 uLysProPheLysCysHisLeuCysAsnTyrAlaCysArgArgAsp 136
      |||||||
560 CCCTCACTGGCCACCTCGAGGACGCTCCGTTGGTAAACCTCACAATGT 609
      |||||||
136 laLeuThrGlyHisLeuArgThrHisSerValGlyLysProHisLysCys 152
      |||||||
610 GGATATTGTGGCCGAGCTATTAACAGCGAAGCTCTTTAGAGGAACATAA 659
      |||||||
153 GlyTyrCysGlyArgSerTyrLysGlnArg***SerLeuGluGluHisL 169
      |||||||
660 AGAGCGCTGCCACAACACTTGTGAAAGCATGGGCGCTTCGGGACACACTGT 709
      |||||||
169 sGluArgCysHisAsnTyrLeuGluSerMetGlyLeuProGly***** 186
      |||||||
710 ACCAGTCAATTAAAGAAAGAACTAGACAGTGAATGCCAGAACACCTG 759
      |||||||
186 **ProValIleLysGluGluThr***His***GluMetAlaGluAspLeu 202
      |||||||
760 TGCAAGATAGGATCAGAGAGATCTCTCGTGTGGACAGACTAGCAAGTAA 809
      |||||||
203 CysLysIleGly***GluArgSerLeuValLeuAspArgLeuAlaSerAs 219
      |||||||
810 TGTGCGCAAAACGTAAGAGCTCTATGCTCAGAAATTTCTTGGGACAAAG 859
      |||||||
219 nValAlaLysArgLysSerSerMetProGlnLysPheLeuGlyAspLys* 236
      |||||||
860 GCCTGTCCGACAGCGCCTACGACAGTGCACAGTACGAGAGGAGACGAA 909
      |||||||
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COUNTRY: USA

1 ATGGATGCTCACCAGGGTCAAGACATGTCTTTCTCATCAGGGAAGAAG 50
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
1 MetAspValAspGluGlnAspMetSerGlnValSerGlyLysGluSe 17
51 CCCCCCTGTAAAGCGATACTCCAGATGAGGGCGGATGAGCCCATGCCGATCC 100
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
17 rProProValSerAspThrProAspGluGlyAspGluProMetProValP 34
101 CGGAGGACCTCTCCACCACTCGGGAGGACACACAAGTCTCAAGAGTGAC 150
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
34 roGluAspLeuSerThrThrSerGlyAlaGlnGlnAsnSerLysSerAsp 50
151 AGAGTCGTGGCCAGTAATGTTAACTAGAGACTCAGAGTGATGAAGAGAA 200
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
51 ArgGlyMetAlaSerAsnValIlysValGluThrGlnSerAspGluGluAs 67
201 TGGGCGTCCTCTGTAATGAATGGGAGAATGTGCGGAGGATTTCAGAA 250
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
67 nGlyArgAlaCysGluMetAsnGlyGluGluCysAlaGluAspLeuArgM 84
251 TGCTTGATGCCTCGGGAGAGAAAATGAATGGCTCCCACAGGAGCACCAAGGC 300
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
84 etLeuAspAlaSerGlyGluLysMetAsnGlySerHisArgAspGlnGly 100
301 AGCTTCGGCTTGTCCGGAGTTGGAGGCAATCGACTTCTTACCGAAAACT 350
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
101 SerSerAlaLeuSerGlyValGlyGlylleArgLeuProAsnGlyLysLe 117

us-08-711-417c-165.ra1

Wed Aug 28 10:05:45 2002

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351 AAAGTGTGATATCTGGGATTCATTCGCGGCCCAATGTGCTCATGG 400
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117 uLysCysAspIleCysGlyValCysIleGlyProAsnValLeuMetV 134
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401 TTCAAAAGAACCACTGGAGAACGCCCTTCAGTGCATCAGTGC 450
|||||
134 alHisLysArgSerHisThrGlyGluArgProPheGlnCysAsnGlnSer 150
|||||
451 GGGGCTCATTCACCCAGAGGCAACCTGCTCCGGCACATCAAGCTGCA 500
|||||
151 GlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuH1 167
|||||
501 TTCCGGGAGAGCCCTCAAAATGCCACCTCTCCAACTAGCGCTGCCGCC 550
|||||
167 sSerGlyGluLysProPheLysCysHisLeuCysAsnTyrAlaCysArgA 184
|||||
551 GGAGGAGCGCCTCAGTGGCCACCTGAGGACGACCTCCGTTGTTGAACCT 600
|||||
184 rArgAspAlaLeuThrGlyHisLeuArgThrHisSer..... 196
601 CACAAATGTGGATATTGTGGCCGAAGCTATAAAGCGGAACGCTTTAGA 650
196 ..... 196
651 GGAACATAAGAGCGCTCCACACTACTTGAAGAGCATGGCTCCGG 700
196 ..... 196
701 GCACACTGTACCCAGTCATTAAGAGAACTAAGCACAGTGAATGGCA 750
196 ..... 196
751 GAAGACCTGTGAAGATAGGATCAGAGATCTCTCGTGTGGACAGACT 800
196 ..... 196
801 AGCAAGTAATGTGCCAAACGTAAGAGCTCTATGCTCAGAAATTTCTTG 850
197 .....G 197
851 GGGACAGAGCGCTGTCGACAGCGCTACGACAGTGCCACGTACGAGAG 900
197 lyAspLysCysLeuSerAspMetProTyrAspSerAlaAsnTyrGluLys 213
901 GAGAACGAAATGATGAGTCCCGTGTGAGGACCAAGCCATCAACAGCG 950
197 ..... 196
214 Glu...AspMetMetThrSerHisValMetAspGlnAlaIleAsnAl 229
951 CATCAACTACTGGGGCGCGGTCCTGCGCGCTGGTGCAGACGCGCC 1000
229 aIleAsnTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThrProp 246
1001 CGGGCGGTTCGAGGTGTCGCGTATCATCAGCCGCGATGACAGCTGCAC 1050
246 roGlySerSerGluValProValIleSerSerMetTyrGlnLeuHis 262
1051 AGG...CGCTGGAGGGACCCCGCTCCCAACCTCCGCGCCAGGACAG 1097
263 LysProSerAspGlyProProArgSerAsnHisSerAlaGlnAsp... 278
1098 CGCGTGGAGTACCTGCTGCTCTCCAGGCCAAGTTGGTCCCTCGG 1147
279 .AlaValAspAsnLeuLeuLeuSerLysAlaLysSerValSerSerG 295
1148 AGCGGAGCGCTCCCGAGCAACAGCTCCCAAGCTCCAGCACACCGAG 1197
295 luArgGluAlaSerProSerAsnSerCysGlnAspSerThrAspThrGlu 311
1198 AGCAACAGCAGGAGGAGCGAGCGGTCTTATCTACCTGACCAACACCAT 1247
312 SerAsnAlaGluGlnArgSerGlyLeuIleTyrLeuThrAsnHisI 328
1248 CGCCCGAGCGCGCAACGC...GTGCTGCTCAAGGAGGAGGACCGCGCT 1294

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328 eAsnProHisAlaArgAsnGlyLeuAlaLeuLysGluGlnArgAlat 345
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1295 AGGACCTGCTGGCGCCCTCCGAGAACTCGCAGGACGCGCTCCGCGTG 1344
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345 yrGluValLeuArgAlaAlaSerGluAsnSerGlnAspAlaPheArgVal 361
|||||
1345 GTCAAGCAGCGGGGAGCAGATGAGGTGTACAGTGCAGAACACTGCGG 1394
|||||
362 valSerThrSerGlyGluGlnLeuLysValTyrLysCysGluHisCysAr 378
|||||
1395 GTGCTCTCTCTGATCAGTTCATGTACACCATCCACATG.....G 1435
|||||
378 gValLeuPheLeuAspHisValMetTyrThrIleHisMetGlyCysHisG 395
|||||
1436 GCTGCCACGCTTCCTGATGCTCTTTGAGTGCACATGTGCGCTTACCAC 1485
|||||
395 LysCysHisGlyPheArgAspPropPheGluCysAsnMetCysGlyTyrHis 411
|||||
1486 AGCAGGACCGGTACGAGTTCCTGTCGACATTAACGAGGAGGAGCAGCG 1535
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412 SerGlnAspArgTyrGluPheSerSerHisIleThrArgGlyGluHisar 428
1536 CTTCACATGAGC 1548
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428 gTyrHisLeuSer 432
seq_name: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:us-08-711-417c-195

seq_documentation_block:
: Sequence 195, Application US/08711417C
: Patent No. 6228611
: GENERAL INFORMATION:
: APPLICANT: Georgopoulos, Katia A.
: TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
: NUMBER OF SEQUENCES: 202
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson P.C.
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: Windows 95
: SOFTWARE: FastSeq for Windows Version 2.0b
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/711,417C
: FILING DATE: 05-Sep-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/238,212
: FILING DATE: 02-MAY-1994
: APPLICATION NUMBER: 08/121,438
: FILING DATE: 14-SEP-1993
: APPLICATION NUMBER: 07/946,233
: FILING DATE: 14-SEP-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Myers, Louis P.
: REGISTRATION NUMBER: 35,965
: REFERENCE/DOCKET NUMBER: 10287/007001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617/542-5070
: TELEFAX: 617/542-8906
: TELEX: 200154
: INFORMATION FOR SEQ ID NO: 195:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 431 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FRAGMENT TYPE: internal

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SEQUENCE DESCRIPTION: SEQ ID NO: 195:
US-08-711-417C-195

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alignment_scores:
  Quality: 1923.50      Length: 521
  Ratio: 4.703          Gaps: 7
  Percent Similarity: 78.503  Percent Identity: 73.129

alignment_block:
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Align seg 1/1 to: US-08-711-417C-195 from: 1 to: 431

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1 MetAspValaspGluGlnaspMetSerGlnValSerGlyLysGlu 17
51 CCCCCCTGAAGGATPACTCCAGATGAGGCGATGAGCCCATGCCGATCC 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17 rProProValSerAspThrProaspGluGlnaspMetProvalP 34
101 CGAGGACCTCTCCACCACTCCGGAGGACAGCAAGCTCCAAGAGTGAC 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 roGluAspLeuSerThrThrSerGlyAlaGlnGlnAsnSerLysSer 50
151 AGAGTCGTGGCCAGTAATGTTAAAGTAGAGACTCAGATGATGAAGAA 200
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51 ArgGlyMet..... 53
201 TGGGGGTGCTGTGAATGAATGGAAGAAATGTGCGGAGGATTTACGA 250
53 ..... 53
251 TCCTTGATGCTCGGAGAGAAATGAATGGCTCCACAGGAGCAAGGC 300
53 ..... 53
301 AGCTCGGCTTTGTCGGGAGTGGAGGCATTCGACTTCCTAACGGAAC 350
53 ..... 53
351 AAAGTGTGATCTGTGGGATCATTTGTCATCGGGCCCAATGTGCTATGG 400
53 ..... 53
401 TTCACAAAGAAGCCACACTCGAAGCGGCTTCCAGTGCAATCAGTGC 450
54 .....GlyGluArgProPheGlnCysAsnGlnSer 63
451 GGGGCTCATTACCCAGAGAGGCAACTGCTCGGCACATCAAGCTGCA 500
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64 GlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisLysLeuH 80
501 TTCGGGAGAGGCTTCAATGCCACCTCTGCAACTACGCCCTGCCGCC 550
80 sSerGlyGluLysProPheLysCysHisLeuCysAsnTyrAlaCys 97
551 GGAGGAGCGCCCTCACTGGCCACCTGAGGAGGCACTCCGTTGGTAAC 600
97 rGArgaspAlaLeuThrGlyHisLeuArgThrHisSerValGlyLys 113
601 CACAAATGTGGATATTGGCCGAGCTATAAAGAGCAAGCTCTTTAGA 650
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114 HisLysCysGlyTyrCysGlyArgSerTyrLysGlnArgSerLeuG 130
651 GGAACATAAAGAGGCTGCCACACTACTTGGAAAGCATGGCCCTCCGG 700
130 uGluHisLysGluArgCysHisAsnTyrLeuGluSerMetGlyLeu 147
701 GCACACTGTACCACTATTAAAGAGAACTAAGCACACTGAAATGGCA 750
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147 ly...ValCysProValLysGluThrAsnHisAsnGluMetAla 162
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751 GAAGACCTGTCCAGATAGGATCAGAGAGATCTCTCGTGTGGACAGACT 800
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163 GluAspLeuCysLysLysLysLysLysLysLysLysLysLysLysL 179
801 AGCAAGTAATGTCCGCAAAACGTAAGAGCTCTATGCTCAGAAATTTCT 850
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179 uAlaSerAsnValAlaLysArgLysSerSerMetProGlnLysPhe 196
851 GGGACAGGGCTGTCCGACACGCGCTTACGACAGTGCACACCTACAGA 900
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
196 lyAspLysCysLeuSerAspMetProTyrAspSerAlaAsnTyrGlu 212
901 GAGAAGAAATGATGATCCAGCTGATGGACCAAGCCATCAACAACGC 950
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213 Glu...AspMetMetThrSerHisValMetAspGlnAlaLysAsn 228
951 CATCAACTACCTGGGGCGAGTCCCTGCGCCCTGCTGTCAGACGCC 1000
228 aLeAsnTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThr 245
1001 CGGCGGCTCCGAGGTGTCCTCCGCTCATCAGCCGCTGATGTCACG 1050
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245 roGlySerSerGluValValProValLysSerSerMetTyrGlnLe 261
1051 AGG...CGCTCGGAGGCGCCCGCTCCCAACCACTCGCGCCAGGAC 1097
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262 LysProProSerAspGlyProProArgSerAsnHisSerAlaGln 277
1098 CGCGCTGGAGTACTGCTGCTGCTCTCCAAAGGCAAGTTGCTGCT 1147
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278 .AlaValAspAsnLeuLeuLeuSerLysAlaLysSerValSerSer 294
1148 AGCGGAGGCTCCCGAGCAACAGCTGCCAAGCTCCAGGACCGACG 1197
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294 luArgGluAlaSerProSerAsnSerCysGlnAspSerThrAspTh 310
1198 AGCAACAACAGGAGGAGCGAGCTGCTTATCTACTGACCAACCA 1247
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311 SerAsnAlaGluGluGlnArgSerGlyLeuLysLeuThrAsnHis 327
1248 CGCGCCGAGCGGCAACGC...GTGCTGCTCAAGGAGGACCGCGCT 1294
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
327 eAsnProHisAlaArgAsnGlyLeuAlaLeuLysGluGlnArgAla 344
1295 ACACCTGTGCTCGCGCGCTCCGAGAACTCGCAGGACGCTCCGCG 1344
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
344 yGluValLeuArgAlaAlaSerGluAsnSerGlnAspAlaPheArg 360
1345 GTCAGCACGCGGGGAGGAGATGAAGTGTACAAGTGCACACTGCG 1394
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361 ValSerThrSerGlyGluGlnLeuLysValTyrLysCysGluHis 377
1395 GTGCTCTCTCTGATCATGTACACCATCCACATG.....G 1435
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
377 gValLeuPheLeuAspHisValMetTyrThrHisMetGlyCysHis 394
1436 GTGCGACCGCTTCCGTGATCTCTTTGAGTGCACATGTCGGCTAC 1485
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394 lyCysHisGlyPheArgAspProPheGluCysAsnMetCysGlyTy 410
1486 AGCGAGGACCGGTACGAGTTCGTCGCGACATAACGCGAGGAGCAC 1535
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
411 SerGlnAspArgTyrGluPheSerSerHisIleThrArgGlyGlu 427
1536 CTCCACATGAGC 1548
|||:|||||:|||||
427 gTyrHisLeuSer 431

seq_name: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:US-08-711-417c-201
seq_documentation_block:
; Sequence 201, Application US/08711417C
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Patent No. 6228611
GENERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 202
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/711.417C
FILING DATE: 05-Sep-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/238,212
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 08/121,438
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis P.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10287/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 201:
SEQUENCE CHARACTERISTICS:
LENGTH: 334 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
SEQUENCE DESCRIPTION: SEQ ID NO: 201:
US-08-711-417C-201

alignment_scores:
Quality: 1740.00 Length: 376
Ratio: 5.210 Gaps: 1
Percent Similarity: 88.830 Percent Identity: 88.830

alignment_block:
US-08-711-417C-165 x US-08-711-417C-201 ..

Align seg 1/1 to: US-08-711-417C-201 from: 1 to: 334

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1 GlyGluArgProPheGlnCysAsnGlnCysGlyAlaSerPheThrGlnLy 17
471 GGCAACCTGTCGGGCACATCAAGCTGCATTCGGGGGAGAACCCCTTCA 520
17 sGlyAsnLeuLeuArgHisIleLysLeuHisSerGlyGluLysProPheL 34
521 AATGCCACCTCTGAACCTACCGCTCGCGGAGGACGCCCTCACCTGGC 570
34 yscYSHisLeuCysAsnTyrAlaCysArgArgAspAlaLeuThrGly 50
571 CACCTGAGGAGCGACTCGCTGGTGGTAAACCTCACAAATGTGGATATGTGG 620
51 HisLeuArgThrHisSer..... 56
621 CGGAAGCTATAACACGCGAAGCTCTTTAGAGGAACATAAGAGCGCTGCC 670

56 56
671 ACAACTACTTGGAAAGCATGGGCTTCCGGGACACACTGTACCCAGTCATT 720
57Valile 58
721 AAAGAAGAACTAAGCACACTGAAATGGCAGAAAGACCTGTGCAAGATAGG 770
59 LysGluGluThrLysHisSerGluMetAlaGluAspLeuCysLysIleG 75
771 ATCAGAGAGATCTCTGCTGTGCACAGACTAGCAAGTAATGTCCGCAAC 820
75 ySerGluArgSerLeuValLeuAspArgLeuAlaSerAsnValAlaLys 92
821 GTAAGACCTCTATGCTCAGAAATTTCTGGGACAAAGGCGCTGTCCGAC 870
92 rgLysSerSerMetProGlnLysPheLeuGlyAspLysGlyLeuSerAsp 108
871 ACGCCCTACGACAGTGCAGTACGAGAGAGAGAAATGATGAAGTC 920
109 ThrProTyrAspSerAlaThrTyrGluLysGluAsnGluMetMetLysSe 125
921 CCAGCTGATGACCAAGCCATCAACACGCCATCACTACTCTGGGGCCG 970
125 rHisValMetAspGlnAlaIleAsnAsnAlaIleAsnTyrLeuGlyAlaG 142
971 AGTCCCTGCGCCGCTGTGTGCAGAGAGCGCGGCGGCTTCGAGGTGTC 1020
142 luSerLeuArgProLeuValGlnThrProGlyGlySerGluVal 158
1021 CCGGTCTACGCGCGATGTACCACTGCACAGCGCTCGGAGGACACCC 1070
159 ProValIleSerProMetTyrGlnLeuHisArgArgSerGluGlyThrPr 175
1071 GCGTCTCAACCACTCGGCCAGGACAGCGCGTGGAGTACCTGCTGTGC 1120
175 oArgSerAsnHisSerAlaGlnAspSerAlaValGluTyrLeuLeuL 192
1121 TCTCCAAGCCCAAGTTGTTGCTCGGAGCGCGGCTCCCGAGCAAC 1170
192 euSerLysAlaLysLeuValProSerGluArgGluAlaSerProSerAsn 208
1171 AGCTGCCAAGACTCCACGACACCGAGAGCAACACAGAGGACGCGGAG 1220
209 SerCysGlnAspSerThrAspThrGluSerAsnAsnGluGluGlnArgse 225
1221 CGGTCTTATCTACCTGACCAACACCATCGCCGCGCGCGCAACGCGTGT 1270
225 rglyLeuIleTyrLeuThrAsnHisIleAlaArgArgAlaGlnArgValS 242
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242 erLeuLysGluGluHisArgAlaTyrAspLeuLeuArgAlaAlaSerGlu 258
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292 yrThrIleHisMetGlyCysHisGlyPheArgAspProPheGluCysasn 308
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seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-711-417C-199

seq_documentation_block:

; Sequence 199, Application US/08711417C

; Patent No. 6228611

; GENERAL INFORMATION:

; APPLICANT: Georgopoulos, Katia A.

; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE

; NUMBER OF SEQUENCES: 202

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: FastSeq for Windows Version 2.0b

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/711,417C

; FILING DATE: 05-Sep-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/238,212

; FILING DATE: 02-MAY-1994

; APPLICATION NUMBER: 08/121,438

; FILING DATE: 14-SEP-1993

; APPLICATION NUMBER: 07/946,233

; FILING DATE: 14-SEP-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Myers, Louis P.

; REGISTRATION NUMBER: 35,965

; REFERENCE/DOCKET NUMBER: 10287/007001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 199:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 390 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: internal

; SEQUENCE DESCRIPTION: SEQ ID NO: 199:

US-08-711-417C-199

alignment_scores:

Quality: 1681.00 Length: 521

Ratio: 4.556 Gaps: 7

Percent Similarity: 70.825 Percent Identity: 65.835

alignment_block:

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34 rogluAspLeuSerThrThrSerGlyAlaGlnGlnAsnSerLysSerAsp 50

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401 TTCACAAAAGAGCCACACTGGAGAACGGCCCTTCCAGTGCATCAAGTGC 450

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54GlyGluArgProPheGlnCysAsnGlnSer 63

451 GGGGCTCATTCACCCAGAGGCAACCTGCTCCGGCACATCAAGCTGCA 500

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64 GlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHi 80

501 TTCGGGGAGAGAGCCCTTCAATGCCACCTCTGCAACTACGCTGCCGCC 550

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80 sSerGlyGluLysProPheLysCysHisLeuLysCysAsnTyrAlaCysArg 97

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551 GGAGGACCGCCTCACTGGCCACCTGAGGAGCGCACTCGCTGGTAAACCT 600

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97 rArgAspAlaLeuThrGlyHisLeuArgThrHisSer..... 109

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651 GGAACATAAGAGCGCTGCCACAACTACTTGGAAAGCATGGCCCTTCGG 700

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122 GluAspLeuLysLysIleGlyAlaGluArgSerLeuValLeuAspArgLe 138

801 AGCAAGTAATGTCCGCAACGTAAGAGCTCTATGCCTCAGAAATTTCTTG 850

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; Sequence 200, Application US/08711417C
; Patent No. 6228611
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 202
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/711,417C
; FILING DATE: 05-Sep-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/238,212
; FILING DATE: 02-MAY-1994
; APPLICATION NUMBER: 08/121,438
; FILING DATE: 14-SEP-1993
```

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;
; APPLICATION NUMBER: 07/946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis P.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10287/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 200:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 376 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 200:
US-08-711-417C-200
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Ratio: 4.565 Gaps: 6
Percent Similarity: 68.330 Percent Identity: 63.724

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901 GAGAACAATATGATGAAGTCCCAAGCTGATGACCAAGCCATCAACAACGC 950
158 Glu...AspMetThrSerHisValMetAspGlnAlaIleAsnAl 173
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173 aileAsnTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThrProp 190
1001 CGGGCGGTTCCGAGGTGGTCCCGGTCATCAGCCGATGACCAGTGCAC 1050
190 roGlySerSerGluValValProValIleSerSerMetTyrGlnLeuHis 206
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seq_documentation_block:

; Sequence 175, Application US/08711417C

; Patent No. 6228611

; GENERAL INFORMATION:

; APPLICANT: Georgopoulos, Katia A.

; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE

; NUMBER OF SEQUENCES: 202

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: FastSeq for Windows version 2.0b

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/711,417C

; FILING DATE: 05-Sep-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/238,212

; FILING DATE: 02-MAY-1994

; APPLICATION NUMBER: 08/121,438

; FILING DATE: 14-SEP-1993

; APPLICATION NUMBER: 07/946,233

; FILING DATE: 14-SEP-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Myers, Louis P.

; REGISTRATION NUMBER: 35,965

; REFERENCE/DOCKET NUMBER: 10287/007001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 175:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 236 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 175:

US-08-711-417C-175

alignment_scores:

Quality: 1210.00

Ratio: 5.216

Length: 236

Gaps: 1

Percent Similarity: 98.305 Percent Identity: 97.881

alignment_block:

US-08-711-417C-165 x US-08-711-417C-175 ..

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seq_documentation_block:
; Sequence 177, Application US/08711417C
; Patent No. 6228611
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 202
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA

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COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/711,417C
FILING DATE: 05-Sep-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/238,212
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 08/121,438
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: 07/946,233
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis P.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10287/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 177:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Other
LOCATION: 1...238
OTHER INFORMATION: Xaa = any amino acid
SEQUENCE DESCRIPTION: SEQ ID NO: 177:
US-08-711-417C-177

alignment_scores:
Quality: 1198.50 Length: 238
Ratio: 5.144 Gaps: 3
Percent Similarity: 97.899 Percent Identity: 97.899

alignment_block:
US-08-711-417C-165 x US-08-711-417C-177 from: 1 to: 238
Align seg 1/1 to: US-08-711-417C-177 from: 1 to: 238
850 GGGACAAAGGCGCTGTCGACAGCGCTAGACAGTCCACGCTACGAGAA 899
|||||
1 GlyAspLysGlyLeuSerAspThrProTyrAspSerAlaThrTyrGlu 17
900 GGAGAACGAATGATGAAGTCCACGATGATGACCAAGCATCAACAACG 949
|||||
17 sGluAsnGluMetMetLysSerHisValMetAspGlnAlaIleAsnAsnA 34
950 CCATCAACTACCTGGGGCCGAGTCCCTGCGCCGCTGGTGGTGCAGACGCC 999
|||||
34 lalleAsnTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThrPro 50
1000 CCGGGCGGTTCCGAGGTGGTCCCGGTCATCAGCCCGATGTACCAAGTGA 1049
|||||
51 ProGlyGlySerGluValProValIleSerProMetTyrGlnLeuH 67
1050 CAGG...CGTTCGAGGCGCACCGCGCTCCAAACCATCGGCCCGCAGACA 1096
|||||
67 sArg**ArgSerGluGlyThrProArgSerAsnHisSerAlaGlnAspS 84
1097 GCGCGGTGGAGTACCTGCTGCTCTCCAAAGGCGCAAGTTGGTGCCTCG 1146
|||||
84 erAlaValGluTyrLeuLeuLeuSerLysAlaLysLeuValProSer 100

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1147 GAGCGGAGGGCTCCCGGAGCAACAGCTGCCAAGACTCCACGGACACCGA 1196
|||||
101 GluArgGluAlaSerProSerAsnSerCysGlnAspSerThrAspThrG1 117
1197 GAGCAACAACAGGAGGAGCGACGCGCTTATCTACCTGACCAACACACA 1246
|||||
117 userAsnAsnGluGluGlnArgSerGlyLeuIleYrLeuThrAsnHisI 134
1247 TGGCCCGCAGCGCGCAACGCC...GTGTGCTCAAGGAGGAGCACCGGCC 1293
|||||
134 leAlaArgAlaGlnArg**ValSerLeuLysGluGluHisArgAla 150
1294 TACGACCTGCTGCGCGCGCTCCGAGAACTCGCAGGAGCGCTCCCGGT 1343
|||||
151 TyrAspLeuLeuArgAlaAlaSerGluAsnSerGlnAspAlaLeuArgVa 167
1344 GGTACGACACCGGGGAGCAGATGAAGGTGTACAAGTGCAGACACTGCC 1393
|||||
167 lValSerThrSerGlyGluGlnMetLysValTyrLysCysGluHisCysA 184
1394 GGTGCTCTTCCTGGATCAGCTCATGTACACCATCCACATG..... 1434
|||||
184 rgValLeuPheLeuAspHisValMetTyrThrIleHisMet***** 200
1435 GGCTGCCACGCTTCCTCGTGATCCTTTGAGTGAACATGTGCGGCTACCA 1484
|||||
201 GlyCysHisGlyPheArgAspPropheGluCysAsnMetCysGlyTyrH1 217
1485 CAGCCAGGACCGGTACGAGTTCTCGTCGACATAACGCGAGGGGAGCAC 1534
|||||
217 sSerGlnAspArgTyrGluPheSerSerHisIleThrArgGlyGluHisA 234
1535 GCTTCCACATGAGC 1548
|||||
234 rgPheHisMetSer 238

